

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 27, 2001, 16:42:23 ; Search time 26.6 Seconds

(without alignments)

933.568 Million cell updates/sec

Title: US-09-483-543A-9
Perfect score: 1733
Sequence: 1 KRGCGAGNFSEERSSWYMR.....SGCGXGLEVLFGQPVKRGXG 326

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68; *
1: pir1; *
2: pir2; *
3: pir3; *
4: pir4; *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%
Result No. Score Query Match Length DB ID

Description
C-Crk - mouse

C-Crk - mouse

C-Species: Mus sp. (mouse)

C-Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999

C-Accesion: I158394

R-Ogawa, S.; Toyoshima, H.; Kozutsumi, H.; Hagiwara, K.; Sakai, R.; Tanaka, T.; Hirai

Oncogene 9, 1669-1679, 1994

A-Title: The C-terminal SH3 domain of the mouse c-Crk protein negatively regulates ty

A-Reference number: I158394; MUID:94239744

A-Accesion: I158394

A-Status: preliminary; translated from GB/EMBL/DDBJ

A-Molecule type: mRNA

A-Residues: 1-304 <RBS>

A-Cross-references: GB:S77408; PIDN:9632866; PIDN:AB30755.1; PID:9632867

C-Gene: c-crk

C-Superfamily: crk transforming protein; SH2 homology; SH3 homology

F:139-187/Domain: SH3 homology <SH3>

RESULT 1
I158394
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C-Species: Mus sp. (mouse)
C-Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
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ALIGNMENTS

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C-Gene: c-crk
C-Superfamily: crk transforming protein; SH2 homology; SH3 homology
F:139-187/Domain: SH3 homology <SH3>

Result No.	Score	Query Match	Length	DB ID	Description
1	1612	93.0	304	2	I158394 C-Crk - mouse
2	1588	91.6	304	2	A450112 C-Crk - chicken
3	1379.5	79.6	305	1	A450112 epidermal growth f
4	1078	62.2	239	2	A46243 CRK-1 - human
5	1052	60.7	204	2	B45022 CRKL protein - hum
6	917.5	52.9	303	2	S58552 SH2/SH3 adaptor pr
7	911.5	52.6	303	2	A44988 trans-forming proto
8	834.5	48.2	259	2	TVFV10 trans-forming proto
9	818.5	47.2	232	1	TVFV10 SH2-SH3 adaptor pr
10	236	13.6	211	2	A46444 growth factor rece
11	224	12.9	217	2	S26050 modular adaptor Gr
12	224	12.9	217	2	A54688 growth factor rece
13	224	12.9	217	2	A43321 growth factor rece
14	218	12.6	217	2	J10664 SH2-SH3 protein se
15	202	11.7	228	2	S25730 1-Phosphatidylinos
16	184	10.6	1291	2	S00656 hypothetical protein
17	102	10.5	1097	2	T31504 1-Phosphatidylinos
18	178	10.3	1290	2	A36466 1-Phosphatidylinos
19	177	10.2	A31317 trans-forming proto		
20	172.5	10.0	839	1	TWHTW hypothetical prote
21	170	9.8	816	2	T17257 transforming proto
22	167	9.6	844	1	TVMWSV adaptor protein in
23	165	9.5	1270	2	T09194 SH2-containing pro
24	164	9.5	1196	2	T14104 dynamin associated
25	161	9.3	1094	2	T13053 Grb-2 related adap
26	158.5	9.1	330	2	JE0376 gene VAV2 protein
27	154.5	8.9	878	2	151940 dynamin associated
28	152.5	8.8	1011	2	T13055 hypothetical prote
29	8.7		334	2	T33836 protein

A45022
CRK-II - human
C:Species: Homo sapiens (man)
C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 20-Jun-2000
C;Accession: A45022
R:Matsuda, M.; Tanaka, S.; Nagata, S.; Kojima, A.; Kurata, T.; Shibusawa, M.
Mol. Cell. Biol. 12, 3482-3489, 1992
A;Title: Two species of human CRK cDNA encode proteins with distinct biological activities
A;Reference number: A45022; MUID:9233437
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-304 <HAR>
A;Cross-references: GB:D10656; NID:9219554; PIDN:BAA01505.1; PID:9219555
A;Experimental source: Placenta
A;Note: sequence extracted from NCBI backbone (NCBIn:108769, NCBIP:108770)
C;Superfamily: crk transforming protein; SH2 homology; SH3 homology
F:113-118/Domain: SH2 homology #status atypical <SH2>
F:139-187/Domain: SH3 homology <SH3>

Query Match 91.6%; Score 1588; DB 2; Length 304;
Best Local Similarity 98.7%; Pred. No. 2.4e-11; Matches 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 AGNFDSEERSSWYGRISRSQEAVALQGRHQVFLVRDSTSSTSPGDYVLSSENSRSHYI 64
Db 2 AGNFSEERSSWYGRISRSQEAVALQGRHQVFLVRDSTSSTSPGDYVLSSENSRSHYI 64
QY 65 INSSGPRPPPSAQOPPGVSPSLRIGDQEDFSLPALLEFKIHYDTTLIEPVARS 123
Db 62 VNSLGPGAGRGGCPGAQLGNPIRFRIGDQEFDSLPSLEFYKIHYDTTLIEPVSR 121
QY 124 SRQSGVILQEQEATYVRALEMDPEMNEDELPFFKGDTIRIKPEEWNNADSEGRC 183
Db 122 SRQSGVILQEQEATYVRALEMDPEMNEDELPFFKGDTIRIKPEEWNNADSEGRC 181
QY 184 MPVYVEKRPASAVSALIGGNGQEGSHFQPLGPGPEPOPYAQPSVNPLNQGPIYA 243
Db 182 MPVYVEKRPASAVSUTTGMDNSHQPPLGPGPECGPYAQPSINTPLNQGPIYA 241
QY 244 RVIQKRPVNAKYDITALALEVGELVKVTKTIVSGWEGECKNGKRGHFPTVHLQDQNPD 303
Db 242 RVIQKRPVNAKYDITALALEVGELVKVTKTIVSGWEGECKNGKRGHFPTVHLQDQNPD 301

QY 304 EDFS 307
Db 302 EDFS 305

RESULT 4

A46243
epidermal growth factor receptor-binding protein GRB-3 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 12-Feb-1999
C;Accession: A46243
R:Margolis, B.; Silvennoinen, O.; Comoglio, F.; Ronnstrand, C.; Skolnik, E.; Ullrich, Proc. Natl. Acad. U.S.A., 89, 8894-8898, 1992
A;Title: High-efficiency expression/cloning of epidermal growth factor-receptor-binding protein
A;Reference number: A46243; MUID:93028373
A;Accession: A46243
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-339 <HAR>
A;Note: sequence extracted from NCBI backbone (NCBIP:115326)
C;Superfamily: crk transforming protein; SH2 homology; SH3 homology
C;Keywords: growth factor receptor
F:44-149/Domain: SH2 homology <SH2>
F:170-218/Domain: SH3 homology <SH3>

Query Match 62.2%; Score 1078; DB 2; Length 239;
Best Local Similarity 99.5%; Pred. No. 2.1e-73; Matches 206; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 AGNFDSEERSSWYGRISRSQEAVALQGRHQVFLVRDSTSSTSPGDYVLSSENSRSHYI 64
Db 33 AGNFSEERSSWYGRISRSQEAVALQGRHQVFLVRDSTSSTSPGDYVLSSENSRSHYI 92
QY 65 INSSGPRPPPSAQOPPGVSPSLRIGDQEDFSLPALLEFKIHYDTTLIEPVARS 124
Db 93 INSSGPRPPPSAQOPPGVSPSLRIGDQEDFSLPALLEFKIHYDTTLIEPVARS 152
QY 125 RGSGVILQEQEATYVRALEFDENGNDDELPFFKGDTIRIKPEEWNNADSEGRC 184
Db 153 RGSGVILQEQEATYVRALEFDENGNDDELPFFKGDTIRIKPEEWNNADSEGRC 212
QY 185 MPVYVEKRPASAVSALIGGNGQEGSHFQPLGPGPEPOPYAQPSVNPLNQGPIYA 211
Db 213 MPVYVEKRPASAVSALIGGNGQEGSHFQPLGPGPEPOPYAQPSVNPLNQGPIYA 239

Query Match 79.6%; Score 1379.5; DB 1; Length 105;

RESULT 5
B45022
CRK-I - human

Q:	C; Species: Homo sapiens (man) C; Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 12-Feb-1999 C; Accession: B45022 R; Matsuda, M.; Tanaka, S.; Nagata, S.; Kojima, A.; Kurata, T.; Shibusawa, M. Mol. Cell. Biol. 12, 3479-3489, 1992	Db 166 KDRGVQMIPFVVER-----LVRSSPHKGHRNRSNSYGIPEFAHQAQPQTIP 215
A; Title: Two species of human Crk cDNA encode proteins with distinct biological activities	A; Reference number: A45022; MUID:9234347	Qy 231 ------TPIPNLNGPIAVVQKRPWAKDPALEVGELVKVIRKINSGW 278
A; Accession: B45022	A; Status: preliminary	Db 216 IPAVSGSPGAATPLPSTONGPVFAKAIOKRVPAYDKIALALEVGDIVKVRMINQW 275
A; Residues: 1-204 <TEN>	A; Molecular type: mRNA	Qy 279 EGECKNGKRGHPPFHVLDDQNPED 305
A; Experimental source: embryonic lung cells	F; 13-18/Domain: SH2 homology <SH2>	Db 276 EGEVNGRKGLPFPHTHKVKEFDQNPED 302
A; Note: sequence extracted from NCBI backbone (NCBIN:108771, NCBIP:108772)	F; 13-18/Domain: SH3 homology <SH3>	
Query Match 60.7%; Score 1052; DB 2; Length 204; Best local Similarity 99.8%; Pred. No. 1; 5e-71; Matches 200; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	RESULT 7 S58352	
Qy 5 AGNFDESEERSSWYWRSLRSQEAVALIQLGQRHGVFLVRSSTSPPGIVLVSNSRVSHYI 64 Db 2 AGNFDESEERSSWYWRSLRSQEAVALIQLGQRHGVFLVRSSTSPPGIVLVSNSRVSHYI 61	S58352 Crk2 adaptor protein - mouse	
Qy 65 INSSGPRPPVPPSPAQOPPGVSPSLRIGDQEFDSLPALEFYKIHLDTTLEPVAR 124 Db 62 INSSGPRPPVPPSPAQOPPGVSPSLRIGDQEFDSLPALEFYKIHWDTTLEBVS 121	C; Species: Mus musculus (house mouse) C; Date: 14-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 16-Jul-1999 C; Accession: S58352 R; de Jong, R.; Haatjela, L.; Voncken, J.W.; Heisterkamp, N.; Groffen, J. submitted to the EMBL Data Library, August 1995	
Qy 125 RQSGGVILRQEEAEVYRALDFNGNDEEDLPKKGDILRDKPEBQWNAEDSEGKRM 184 Db 122 RQSGGVILRQEEAEVYRALDFNGNDEEDLPKKGDILRDKPEBQWNAEDSEGKRM 181	A; Description: Tyrosine phosphorylation of murine Crk1.	
Qy 185 TPVPPVVEYKRPASAVSVALIGG 206 Db 182 TPVPPVVEYKRPASAVSVALIGG 203	A; Reference number: S58352 A; Accession: S88352 A; Status: preliminary	
RESULT 6 S41754	A; Molecular type: mRNA	
CrkL protein - human	A; Residues: 1-303 <TEN>	
C; Species: Homo sapiens (man)	A; Cross-references: EMBL:X90648; NID:9945008; PIDN:CAA62220.1; PID:9945009	
C; Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999	C; Superfamily: crk transforming protein; SH2 homology; SH3 homology	
R; ten Hoeve, J.; Morris, C.; Heisterkamp, N.; Groffen, J.	F; 13-102/Domain: SH2 homology <SH2>	
A; Title: Isolation and chromosomal localization of CrkL, a human crk-like gene.	F; 13-102/Domain: SH3 homology <SH3>	
A; Reference number: S41754; MUID:93368949	Query Match 52.6%; Score 911.5; DB 2; Length 303; Best Local Similarity 56.0%; Pred. No. 7.7e-61; Matches 183; Conservative 34; Mismatches 57; Indels 53; Gaps 6;	
A; Accession: S41754	Qy 5 AGNFDESEERSSWYWRSLRSQEAVALIQLGQRHGVFLVRSSTSPPGIVLVSNSRVSHYI 64 Db 3 SARFDSSDRSIIWYMGVTROEAFORLQGQRHGMFLVRSSTSPPGIVLVSNSRVSHYI 62	
A; Status: preliminary	Qy 65 INSSGPRPPVPPSPAQOPPGVSPSLRIGDQEFDSLPALEFYKIHLDTTLEPVAR 123 Db 63 INSPLNR-----RFKIGDQEFDHPLALLEFYKIHLDTTLEPARY 105	
A; Molecular type: DNA	Qy 124 -----SRQSGGVILRQEEAEVYRALDFNGNDEEDLPKKGDILRDKPEBQWNAED 177 Db 106 PSPPGVGSVAPNLPTAENLYEVRLDFPGNDADLPKKGDILRDKPEBQWNAED 165	
A; Residues: 1-303 <TEN>	Qy 178 SEGKRMIPVPPVVEYKRPASAVSVALIGGNGEGSH---PQPLGGPERG-PYAOQSVNP 232 Db 166 KDGKVQMPVPPVVEK-----LVRSSPHKGHRNRSNSYGIPEPRAVQAPQTIP 215	
A; Cross-references: EMBL:X59656; NID:9416519; PIDN:CAA42199.1; PID:9416520	Qy 233 LPNL-----OQGPIAVVIRVNPWAKDPALEVGELVKVTKINSGW 278 Db 216 LPTVASTPGAAANPLFSTONGPVFAKAIOKRVPACYDKITALALEVGDIVKVRMINQW 275	
C; Superfamily: crk transforming protein; SH2 homology; SH3 homology	Qy 279 EGECKNGKRGHPPFHVLDDQNPED 305 Db 276 EGEVNGRKGLPFPHTHKVKEFDQNPED 302	
F; 13-10-178/Domain: SH3 homology <SH3>	RESULT 8 A44988	
Query Match 52.9%; Score 917.5; DB 2; Length 303; Best Local Similarity 56.6%; Pred. No. 2.7e-61; Matches 185; Conservative 33; Mismatches 56; Indels 53; Gaps 6;	C; Species: avian sarcoma virus C; Date: 28-Apr-1993 #sequence_revision 14-May-1993 #text_change 07-May-1999 C; Accession: A44988 R; Tsuchie, H.; Chang, C.H.W.; Yoshida, M.; Vogt, P.K. Oncogene 4, 1281-1284, 1989	
Qy 5 AGNFDESEERSSWYWRSLRSQEAVALIQLGQRHGVFLVRSSTSPPGIVLVSNSRVSHYI 64 Db 3 SARFDSSDRSIIWYMGVTROEAFORLQGQRHGMFLVRSSTSPPGIVLVSNSRVSHYI 62	A; Title: A newly isolated avian sarcoma virus, ASv-1, carries the crk oncogene.	
Qy 65 INSSGPRPPVPPSPAQOPPGVSPSLRIGDQEFDSLPALEFYKIHLDTTLEPVAR 123 Db 63 INSPLNR-----RFKIGDQEFDHPLALLEFYKIHLDTTLEPARY 105		
Qy 124 -----SRQSGGVILRQEEAEVYRALDFNGNDEEDLPKKGDILRDKPEBQWNAED 177		

A;	Reference number: A44988; MUID:90045469	Db	209	MIPVYVEKRDSSASVSTLTGG 231
A;Accession:	A44988			
A;Status:	preliminary	RESULT	10	
A;Molecule type:	DNA			
A;Residues:	1-259 <TSU>			
A;Cross-references:	GB:X17292			
A;Title:	the authors translated the codon CGG for residue 79 as GIV, and CAG for residue C;Superfamily:	crk transforming protein; SH2 homology; SH3 homology		
C;Domain:	SH2 homology <SH2>			
F;67-173	Domain: SH3 homology <SH3>			
F;194-242	Domain: SH3 homology <SH3>			
Query Match	48.2%; Score 834.5; DB 2; Length 259;			
Best Local Similarity	78.3%; Pred. No. 3.5e-55;			
Matches	159; Conservative 17; Mismatches 26; Indels 1; Gaps 1;			
Qy	5 AGNIDSEERSSWYWGRSLRSQEAVALLQORGHGVFLVYDSDSTSPPGDYVLSVSENSRSHYI 64			
Db	56 AGQFDSEDRGSWVWGRSLRSQDANVSLLQRERRHGTFLYDRSGSIPPGDVLVSSESRVSHYI 115			
Qy	65 INSSGPRPVPPPAQP-PPGVSRSRIGQDFDSLPALEFFYKHLDTTIEPVAR 123			
Db	116 VNLGPAGSRGRAGEGPGAPGLNPTRFRIGQDFEDSLPSLLEFYKHLDTTIEPVSR 175			
Qy	124 SRQSGVILRQERAEYVRALEDFENGNDDEUDLPFKKGDLIRDKPESQWNAEDESGKRG 183			
Db	176 SRONSGVILOEVNEYVRALEDFENGNDDEUDLPFKKGDLIRDKPESQWNAEDEMDGKRG 235			
Qy	184 MIPVYVEKRYRPASVASVALIGG 206			
Db	236 MIPVYVEKCRPSASAVSVALIGG 258			
RESULT	9			
TVFV10	transforming protein crk - avian sarcoma virus CT10			
C;Species:	avian sarcoma virus CT10			
C;Accession:	B29851			
C;Title:	A novel viral oncogene with structural similarity to phospholipase C.			
A;Reference number:	S00872; MUID:88156964			
A;Accession:	B29851			
A;Molecule type:	genomic RNA			
A;Residues:	1-232 <MAY>			
A;Cross-references:	EMBL:Y00302			
C;Genetics:				
A;Gene:	crk			
C;Superfamily:	crk transforming protein; SH2 homology; SH3 homology			
F;5-53	Domain: SH3 homology <SH3>			
F;60-149	Domain: SH2 homology <SH2>			
Query Match	47.2%; Score 818.5; DB 1; Length 232;			
Best Local Similarity	77.3%; Pred. No. 4.8e-54;			
Matches	157; Conservative 16; Mismatches 29; Indels 1; Gaps 1;			
Qy	5 AGNIDSEERSSWYWGRSLRSQEAVALLQORGHGVFLVYDSDSTSPPGDYVLSVSENSRSHYI 64			
Db	29 AGQFDSEDRGSWVWGRSLRSQDANVSLLQRERRHGTFLYDRSGSIPPGDVLVSSESRVSHYI 88			
Qy	65 INSSGPRPVPPPAQP-PPGVSRSRIGQDFDSLPALEFFYKHLDTTIEPVAR 123			
Db	89 VNLGPAGSRGRAGEGPGAPGLNPTRFRIGQDFEDSLPSLLEFYKHLDTTIEPVSR 148			
Qy	124 SRQSGVILRQERAEYVRALEDFENGNDDEUDLPFKKGDLIRDKPESQWNAEDESGKRG 183			
Db	149 SRONSGVILOEVNEYVRALEDFENGNDDEUDLPFKKGDLIRDKPESQWNAEDEMDGKRG 208			
Qy	184 MIPVYVEKRYRPASVASVALIGG 206			
Qy	: 11 206			
RESULT	11			
Qy	5 AGNIDSEERSSWYWGRSLRSQEAVALLQORGHGVFLVYDSDSTSPPGDYVLSVSENSRSHYI 64			
Db	29 AGQFDSEDRGSWVWGRSLRSQDANVSLLQRERRHGTFLYDRSGSIPPGDVLVSSESRVSHYI 88			
Qy	65 INSSGPRPVPPPAQP-PPGVSRSRIGQDFDSLPALEFFYKHLDTTIEPVAR 123			
Db	89 VNLGPAGSRGRAGEGPGAPGLNPTRFRIGQDFEDSLPSLLEFYKHLDTTIEPVSR 148			
Qy	124 SRQSGVILRQERAEYVRALEDFENGNDDEUDLPFKKGDLIRDKPESQWNAEDESGKRG 183			
Db	149 SRONSGVILOEVNEYVRALEDFENGNDDEUDLPFKKGDLIRDKPESQWNAEDEMDGKRG 208			
Qy	184 MIPVYVEKRYRPASVASVALIGG 206			
Qy	: 11 206			
A;Status:	preliminary			

A; Molecule type: mRNA
A; Residues: I-217 <MAT>
A; Cross-references: EMBL:X62853; NID:955762; PID:955763
R; Watanabe, K.; Fukuchi, T.; Hosoya, H.; Shirasawa, T.; Matuoka, K.; Miki, H.; Takenawa, J. Biol. Chem. 270, 13733-13739, 1995
A; Title: Splicing isoforms of rat AshGrb2. Isolation and characterization of the cDNA.
A; Reference number: 155429; MUID:95293967
A; Accession: 155429
A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: I-156-171-217 <RES>
A; Cross-references: GB:D49846; NID:914956; PIDN:BAA08645.1; PID:9914957
A; Accession: 170120
A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: I-59 <RE2>
A; Cross-references: GB:D49847; NID:914960; PIDN:BAA08646.1; PID:9914961
C; Superfamily: crk transforming protein; SH2 homology; SH3 homology
C; Keywords: growth factor receptor
F; 5'-53/Domain: SH3 homology <SH3>
F; 60-150/Domain: SH2 homology <SH2>
F; 163-210/Domain: SH3 homology <SH3>

Query Match 12.9%; Score 224; DB 2; Length 217;
Best local similarity 27.9%; Pred. No. 1e-09;
Matches 53; Conservative 44; Mismatches 57; Indels 36; Gaps 7;

QY 7 NFDSEERSSSWYGRLSQEAVALLOQGQRH-GVFLVRDSTSSTPGDVYLVSSENRSVSHYT 65
Db 111 LRDG-----AGKYLEWVVKFRISLNELWDYR----STS---VSRNQ 144
Db 126 QGSGLVLRQ---EAEAVRLDFNGNDEEDLPFKKGDIRIRDKPPEQWNAESEG 180
Db 145 Q---IFLRDIEQMFOQPTIVQALFDFDQEDGELGFRRGDFHVMNDSPNWKGAGCHG 200
QY 181 KRGMPFPVY 190
Db 201 QTGMFPRNYV 210

RESULT 13
A43321
growth factor receptor-bound protein 2 - human
N; Alternate names: abundant-src-homology (ash) protein
N; Contains: growth factor receptor-bound protein 3-3
C; Species: Homo sapiens (man)
C; Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C; Accession: A43321; A54064; A46278
R; Lowenstein, E.J.; Daly, R.J.; Batzer, A.G.; Li, W.; Margolis, B.; Lamers, R.; Ullrich, Cell 70, 431-442, 1992
A; Title: The SH2 and SH3 domain-containing protein GRB2 links receptor tyrosine kinases
A; Reference number: A43321; MUID:92354060
A; Accession: A43321
A; Molecule type: mRNA
A; Residues: I-217 <LOW>
A; Cross-references: GB:M96995; NID:918197; PIDN:AA58448.1; PID:9181976
A; Experimental source: brain
A; Note: sequence extracted from NCBI backbone (NCBIPN:110294, NCBITP:110295)
R; Fath, I.; Schweighoffer, F.; Rey, I.; Milton, M.C.; Boizlau, J.; Duchesne, M.; Tocque, Science 264, 971-974, 1994
A; Title: Cloning of a Grb2 isoform with apoptotic properties.
A; Reference number: A54064; MUID:94233382
A; Accession: A54064
A; Molecule type: mRNA
A; Residues: I-59, 101-217 <FAT>
A; Cross-references: GB:L2951; NID:9460667; PIDN:AAQ37549.1; PID:9498178
R; Matuoka, K.; Shibata, M.; Yamakawa, A.; Takenawa, T.
A; Title: Cloning of ASH, a ubiquitous Protein composed of one Src homology region (SH1)
A; Reference number: S26050; MUID:93028395
A; Accession: A46278
A; Molecule type: mRNA
A; Residues: 58-217 <MAT>
A; Cross-references: EMBL:X62852; NID:928875; PIDN:CAA44664.1; PID:928876
C; Genetics:
A; Gene: GDB:GRB2
A; Cross-references: GDB:134732; OMIM:600180
A; Map position: 17q24-17q25
C; Superfamily: crk transforming protein; SH2 homology; SH3 homology
F; 1-217/Product: growth factor receptor
F; 1-59, 101-217/Product: growth factor receptor
F; 5'-53/Domain: SH2 homology <SH2>
F; 60-150/Domain: SH3 homology <SH3>
F; 163-210/Domain: SH3 homology <SH3>

Query Match 12.9%; Score 224; DB 2; Length 217;
Best Local Similarity 27.9%; Pred. No. 1e-09;
Matches 53; Conservative 44; Mismatches 57; Indels 36; Gaps 7;

QY 7 NFDSEERSSSWYGRLSQEAVALLOQGQRH-GVFLVRDSTSSTPGDVYLVSSENRSVSHYT 65
Db 51 NIEMKPHWFEGKIPRAKEEMSLSKORHDGAFLIRESESAPGDFESLSVKFGNDVQHFKV 110
Db 66 NSSGRPPVPPSPAQPPGVSPSLRIGQDFEDSLPALEFFKIHLDTTIJEVARS 125
QY 126 QGSGLVLRQ---EAEAVRLDFNGNDEEDLPFKKGDIRIRDKPPEQWNAESEG 180
Db 145 Q---IFLRDIEQMFOQPTIVQALFDFDQEDGELGFRRGDFHVMNDSPNWKGAGCHG 200
QY 181 KRGMPFPVY 190
Db 201 QTGMFPRNYV 210

RESULT 12
A4688
modular adaptor Grb2 - mouse
C; Species: Mus musculus (house mouse)
C; Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 21-Jan-2000
C; Accession: A54688
R; Suen, K.L.; Bustelo, X.R.; Pawson, T.; Barbacid, M.
Mol. Cell. Biol. 13, 5500-5512, 1993
A; Title: Molecular cloning of the mouse grb2 gene: differential interaction of the Grb2
A; Reference number: A54688; MUID:93360985
A; Accession: A54688
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: I-127 <SUE>
A; Cross-references: GB:U07617; NID:9464004; PIDN:AAB40022.1; PID:9464005
C; Genetics:
A; Gene: grb2
C; Superfamily: crk transforming protein; SH2 homology; SH3 homology
F; 5'-53/Domain: SH2 homology <SH2>
F; 60-150/Domain: SH2 homology <SH2>
F; 163-210/Domain: SH3 homology <SH3>

Query Match 12.9%; Score 224; DB 2; Length 217;
Best Local Similarity 27.9%; Pred. No. 1e-09;
Matches 53; Conservative 44; Mismatches 57; Indels 36; Gaps 7;

QY 7 NFDSEERSSSWYGRLSQEAVALLOQGQRH-GVFLVRDSTSSTPGDVYLVSSENRSVSHYT 65
Db 51 NIEMKPHWFEGKIPRAKEEMSLSKORHDGAFLIRESESAPGDFESLSVKFGNDVQHFKV 110
Db 66 NSSGRPPVPPSPAQPPGVSPSLRIGQDFEDSLPALEFFKIHLDTTIJEVARS 125

Db 111 LRDG-----AGKYFLWVVKFNLSNLVELVDYHR----STS---VSRNQ 144
 A; Reference number: z18361
 Qy 126 QCGSVTIRQ----EREYVRAFLDFNGNDEDDLPKKGDILRKPEQWMWADSEG 180
 A; Accession: T15499
 A; Status: preliminary; translated from GB/EMBL/DDBJ
 C; Species: *Gallus gallus* (chicken)
 C; Alternative names: sex-muscle-abnormal protein 5 (sem-5)
 C; Cross-references: EMBL:U29082; NID:9861384; PID:9861389; PIDN:AAA68405.1
 C; Experimental source: Strain Bristol N2
 A; Cross-references: EMBL:U29082; NID:9861384; PID:9861389; PIDN:AAA68405.1
 A; Residues: 1-228 <MIN>
 A; Molecule type: DNA
 A; Gene: sem-5
 A; Status: preliminary; translated from GB/EMBL/DDBJ
 A; Cross-references: EMBL:U29082; NID:9861384; PID:9861389; PIDN:AAA68405.1
 A; Residues: 1-228 <MIN>
 Db 181 KRGMIPVPPV 190
 A; Accession: JT0664
 Db 201 QMGMFPRNVV 210
 A; Description: The sequence of *C. elegans* cosmid C14F5.

RESULT 14

JT0664 growth factor receptor-binding protein GRB2 homolog - chicken

C;Species: *Gallus gallus* (chicken)
 C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 21-Jan-2000
 C;Accession: JT0664
 A;Title: Sequence of a chicken cDNA encoding a GRB2 protein.
 A;Reference number: JT0664; MUID:94085795
 A;Accession: JT0664
 A;Molecule type: mRNA
 A;Residues: 1-217 <WAS>
 A;Cross-references: GB:L19258; NID:9304385; PIDN:AA16318.1; PID:9304386
 C;Comment: GRB2 protein plays a role in mediating the critical linkage between growth fa
 C;Superfamily: crk transforming protein; SH2 homology; SH3 homology
 C;Keywords: growth factor receptor
 F;5-53/Domain: SH3 homology <SH31>
 F;60-151/Domain: SH2 homology <SH2>
 F;161-208/Domain: SH3 homology <SH32>

Query Match 12.6%; Score 218; DB 2; Length 217;
 Best Local Similarity 27.9%; Pred. No. 2.9e-09;
 Matches 53; Conservative 44; Mismatches 57; Indels 36; Gaps 7;

Qy 7 NFDSEERSSWWGRSLRSQEAVALLQQQRH-GVFLYRDSSTSPGDYVLVSENSRSHVII 65
 Db 51 NYIEMKPHWFRKGKIPRAKAEMLGKORHDGAFLIRESESAPGDFSLSVKFGNDYQFKV 110
 Qy 66 NSSGPRPPVPPSPAQPPPGVSFSRLRIGDQEFDSLPALEFFYKIHLDTTTLIEVARSR 125
 Db 111 LRDG-----AGKYFLWVVKFNLSNLVELVDYHR----STS---VSRNQ 144
 Qy 126 QCGSVTIRQ----EREYVRAFLDFNGNDEDDLPKKGDILRKPEQWMWADSEG 180
 Db 145 Q----IFLRDIEQVPOQPTYVQALFDPQEEGELGRGRGDPQVLDNSDNWWKCA-CHG 200
 Qy 181 KRGMIPVPPV 190
 Db 201 QMGMFPRNVV 210

RESULT 15

S25730 SH2-SH3 protein sem-5 - *Caenorhabditis elegans*
 A;Molecule type: mRNA
 A;Residues: 1-228 <CLIA>
 A;Cross-references: GB:S89446; NID:9247604; PID:9247605
 R;Minx, P.
 A;Description: The sequence of *C. elegans* cosmid C14F5.

Search completed: September 27, 2001, 16:42:24
 Job time: 192 sec

Thu Sep 27 16:46:10 2001

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